

FIG.1

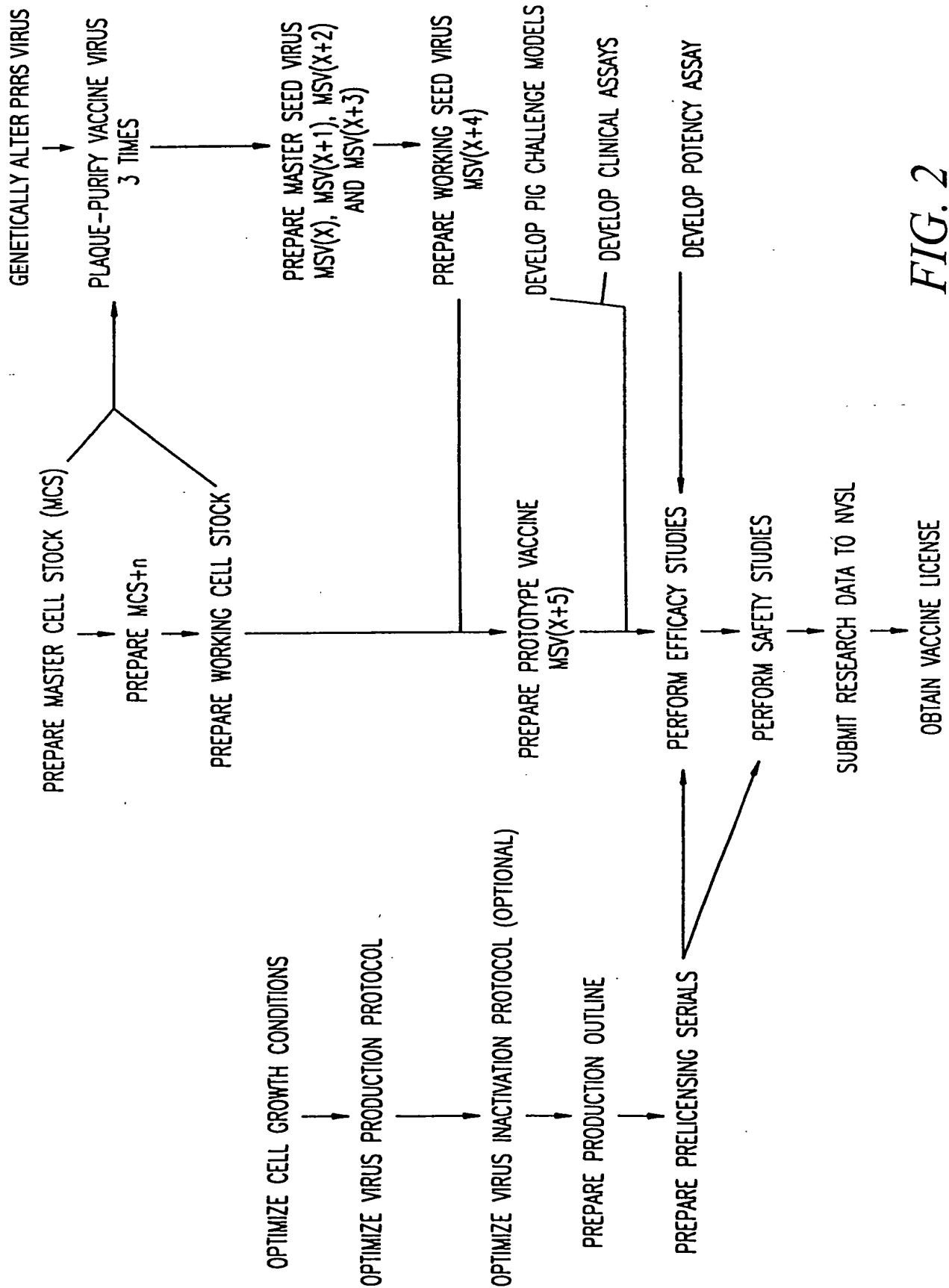


FIG. 2

FIG. 3A

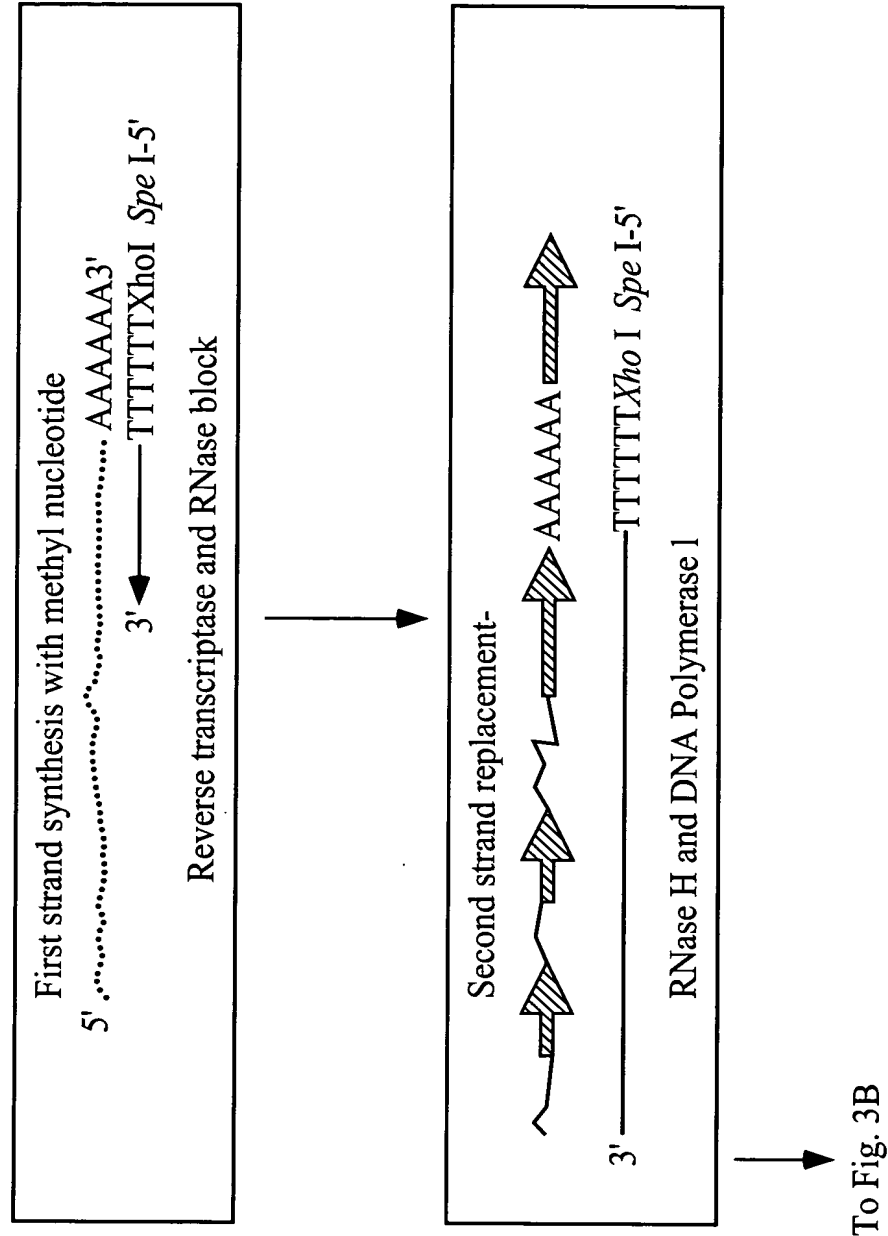
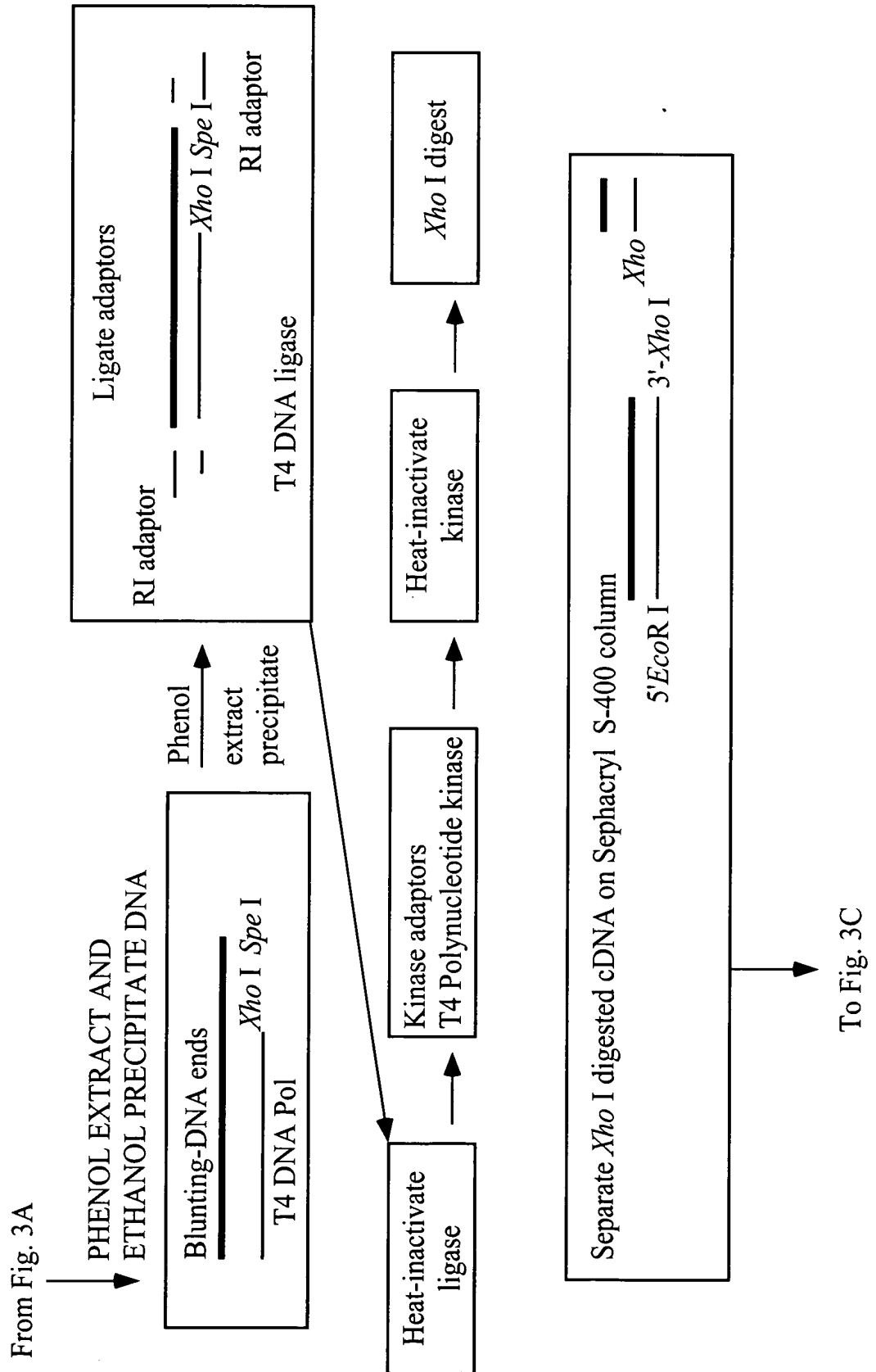


FIG. 3B



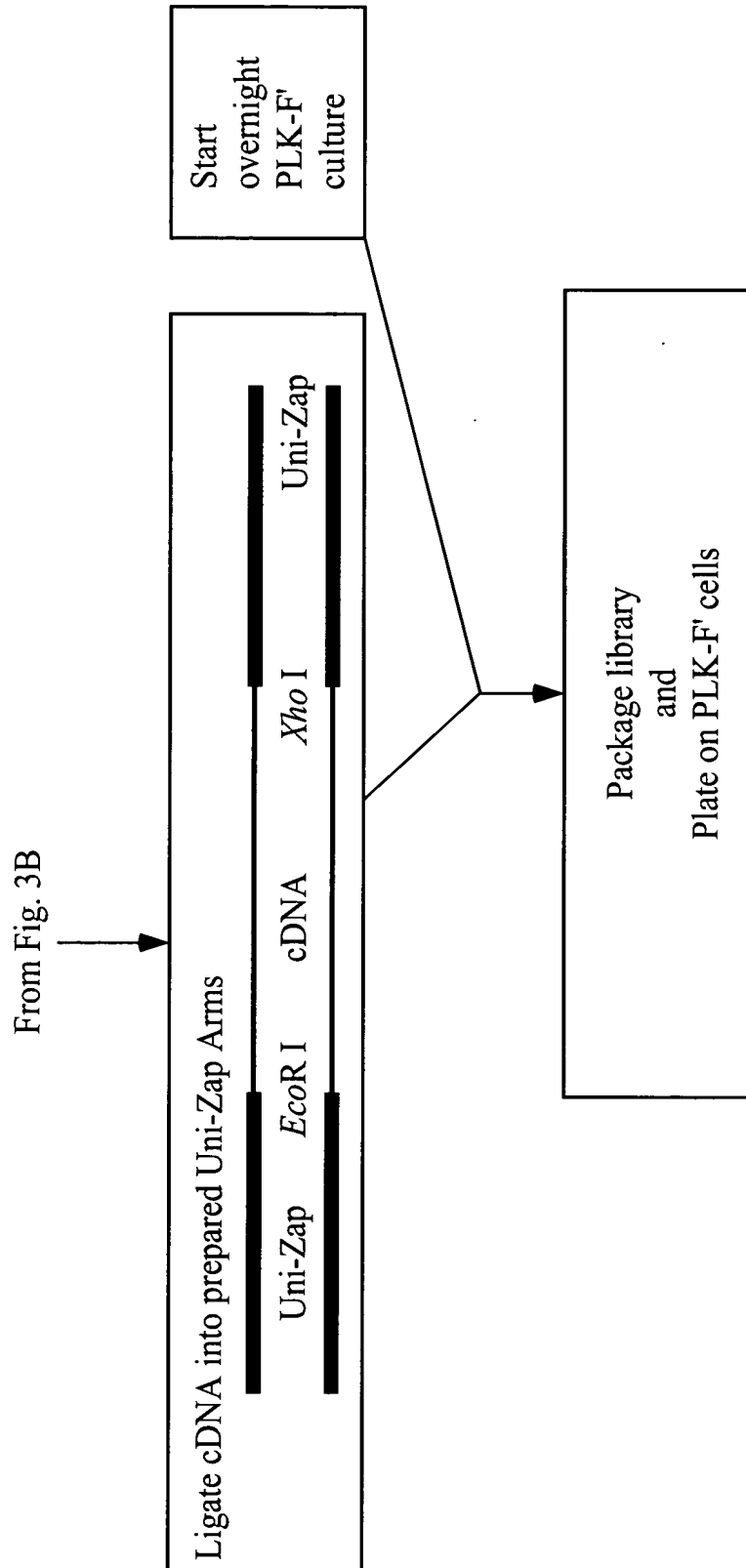


FIG. 3C

Identification of ISU-12 Authentic Clones by Differential Hybridization

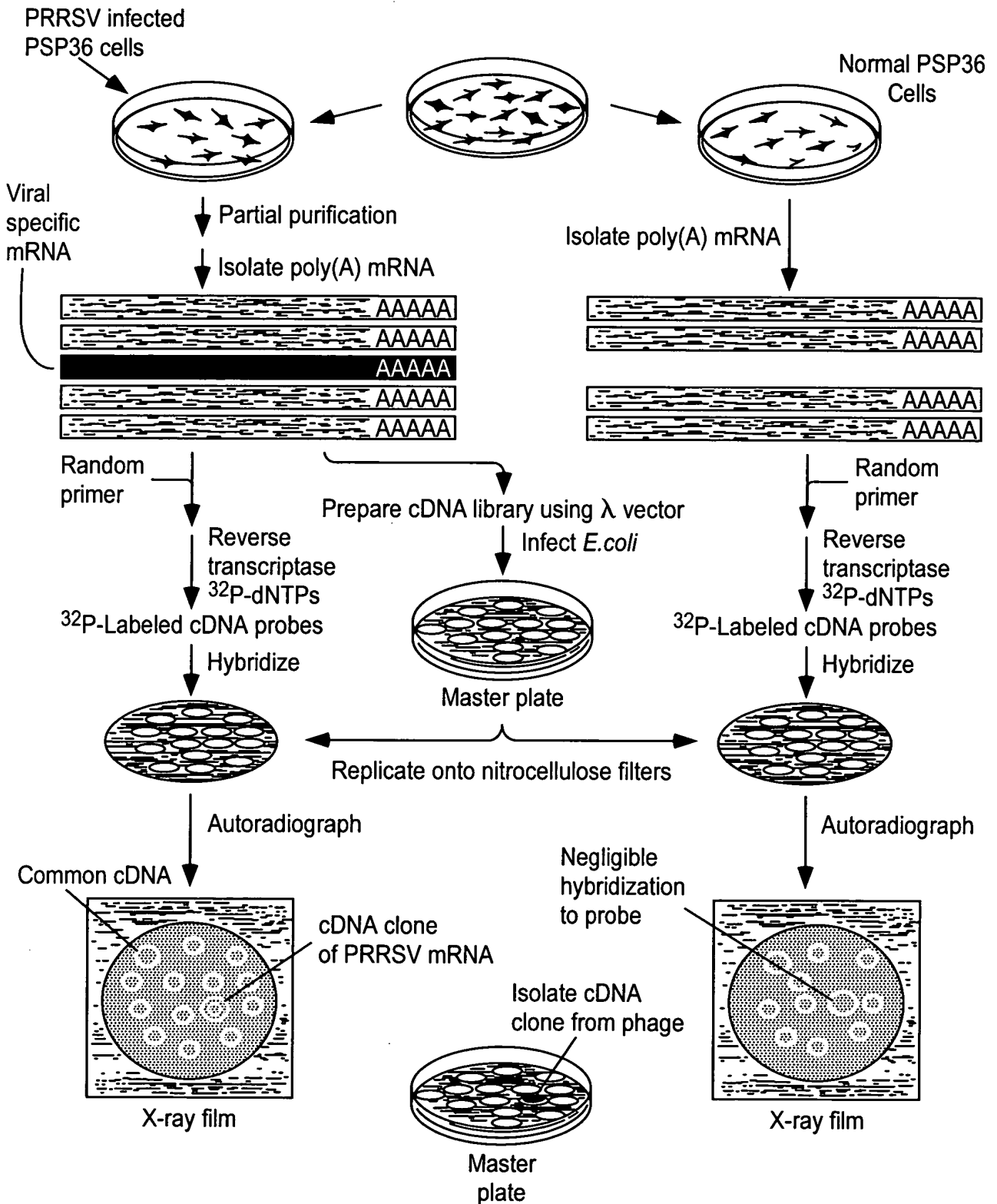


FIG. 4

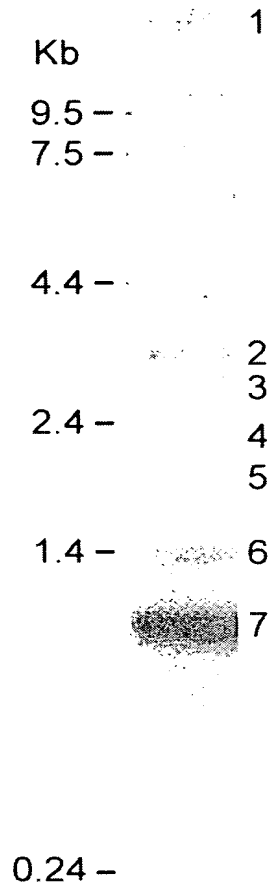


FIG. 5

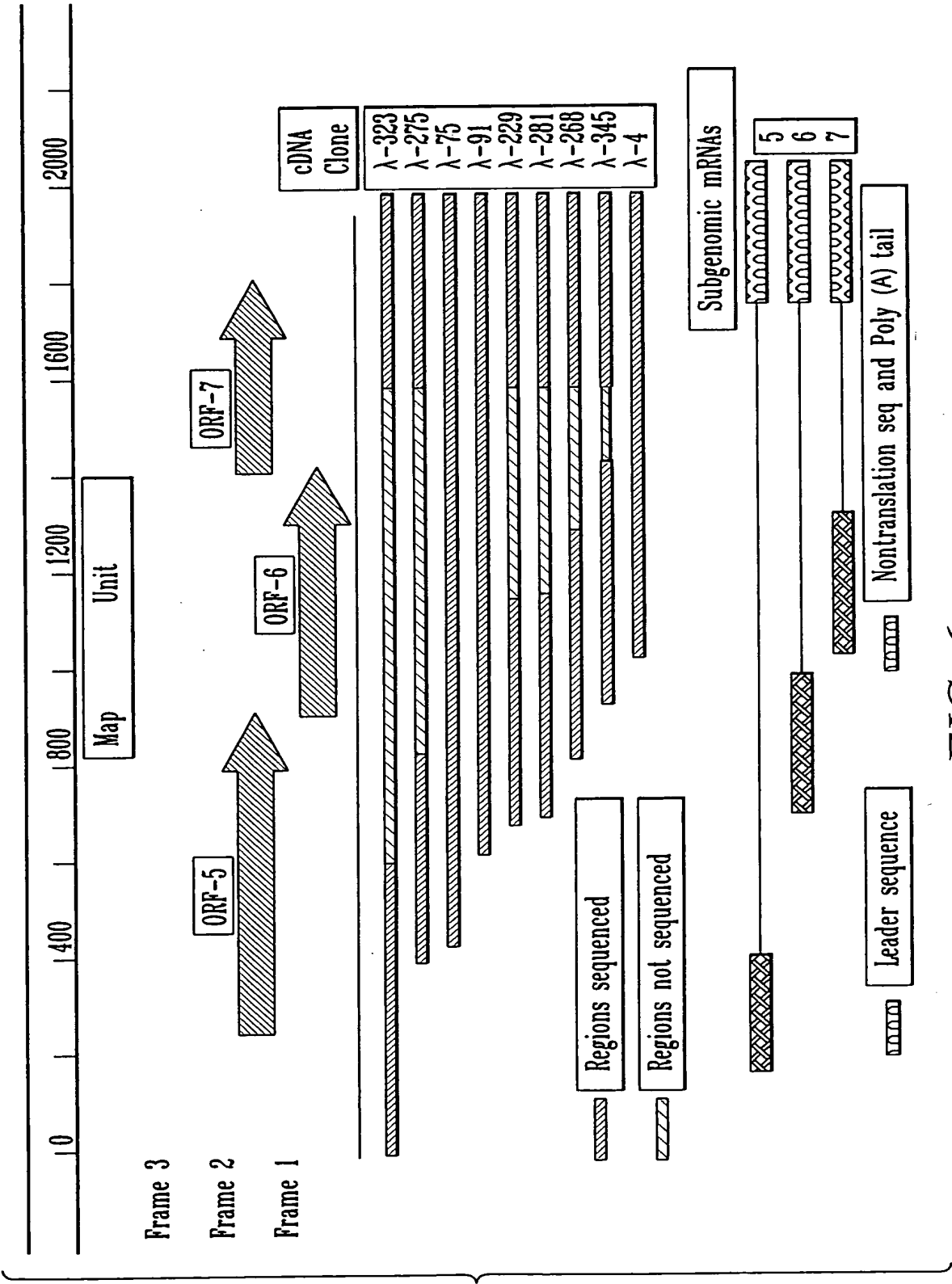


FIG. 6

GGCAGGCTTGGCTCCTCCAAGACATCAGTTGCCCTTAGGCATCGCAACTCGGCCCTGAGGCGATTGCGAAAGTCCTCAGTGGCGCAGGGGATAGGG 100
ACACCCGTGTATACATGTCACAGCCAAATGTTACCGATGAGAAATTATTTGCATTCCTCTGATCTTCTCATGCTTCTTCTTGGCTTTTCTATGCTTCTG 200
AGATGAGTGAAAAGGATTTAAGGTGGTATTTGGCAATGTCTCAGGCATCGTGGCAGTGTGGCTCAACTTACCAGTTACGTCCAACATGTCAGGGAATT 300
TACCAACGTTCCCTGGTAGTTGACCATGTGGGGCTGCTCCATTTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTAGCCCTGCTTTTTTGGCATT 400
CTGTTGGCAATTGAAATGTTAAGTATGTTGGGAAAATGCTTGACCGGGGGCTGTTGCTCGCAATTGCTTTTTTTGGTGTATCGTGCCGCTTGTGTTTT 500
GTTGGCGCTCGTCAGCGCCCAACGGGAACAGCGGCTCAAATTTACAGCTGATTTACAACCTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
AATTTGACTGGGCAGTGGAGTGTTTTGTGATTTTTCCTGTGTTGACTCACATTTGCTCTTATGGTGCCCTCACTACTAGCCATTCTTGGACACAGTCGG 700
TCTGGTCACGTGCTACCGCTGGGTTGTTACCGGGGGTATGTTCTGAGTAGCATGACGGGCTGTGCCCCTGGCTGGCTTGTGATTGCTTCGTCATT 800
AGGCTTGGGAAGAATTGCATGTCTGGCGCTACTCATGTACCAGATATACCAACTTCTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGGCTG 900
TCATCATAGAGAAAAGGGGCAAAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAGAGTTGTGCTTGTATGGTTCCGGGGCTACCCCTGTAACCAAGAGT 1000
TTCAGCGGAACAATGGAGTCGTCCTTAGATGACTTCGTGTCATGATAGCAGGCTCCACAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGA 1100

DRF4 stop

+1>DRF5 start

DRF6 start
+1> ***DRF5 stop

FIG. 7A

TGATATGCCCTAAAGGTAGTCGCGCGGCGACTGCTAGGGCTTCGACACCTTTGGICTCCIGAATTGTGCTTTCACCTTCGGGTACATGACATTGCT 1200
GCACCTTCAGAGTACAAATAAGGTCGCGCTCACAATGGGAGCAGTAGTTGCACCTCCTTTGGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300
TCCAGATGCCGTTTGTGCTTGTAGCGCGCAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGCCGAGGCTTTCATCCGATTGCGGCAATGATA 1400
ACCACGCATTTGTGTCGCGCGTCCCGCTCCACTACGGTCAACGGCACATTGGTGCCCGGTTAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAA 1500
ACAGGGAGTGGTAACCTTGTAAATATGCCAAATAACCCGCAAGCAGAGAGAGAAAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600
GCTGGGTAGATCATCGCTACCCAAACCAGTCCAGAGGCAAGGACCGGAAAGAAAAATAAGAAGAAAAACCCGGAGAGGCCCATTTCCCTCTAGCG 1700
ACTGAAGATGATGTAGACATCACTTTACCCCTAGTGAGCGTCAATTGTGCTGCTCAATCCAGACCGCTTTAATCAAGGCGCTGGGACTTGCACCC 1800
TGTGAGATTCAGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCCTACGCATCATACGTGCGCCTGATCCGGCTCACAGCATCACCTCAGCATGATG 1900
GGCTGGCATTCCTTGAGGCATCCAGTGTGTGAATTGGGAAGATGCGTGGTGAATGGCACGTGATTGACATTGTGCCCTTAAGTCACCTATTCAATTAGGGC 2000
GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACGCGGAAATTAAAAAATAAAAAA 2062

DRF7 start
+1> ***DRF6 stop
***DRF7 stop

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATTGGGGCGTTCCTTGACTCCGCACCTCTTGCCTCTGGTGGCTTTTTTGTGCTGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTTGGGGAAATCCTTGACCCTGGCTCTTGCCTGCCAATTCCTTTTTTGTGGTGATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCCTGGT-DCTTTCCGATGGCAACGGCCACAGCTCGACATACCAATA-C-ATAATATAACTTGG	13624
ISU-12-3' TERMINAL (426-1028)	GTCCGCTCTTGTTTGTTGGGCTAGCGCCAACGGGAACAGCGGCTCAAAATTACAGCTGATTTACAACATTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGCGAGCTGAATGGACCGACTGGTTTGTCAGCCCATTTTGGTTGGGCAGTGGAGACCTTTGTGGTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAATGGACAGATTGGCTAGCTTAATAWATTTGACITGGGCAGTGGAGTGTTTTGTGCATTTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTGGCCACTCATTCCTCTCACTGGGTTTCTCACAAAGCCATTTTGTGACGGCTCGGTCCTGGGCT	13774
ISU-12-3' TERMINAL (426-1028)	CCTGTGTTGACTCACAATTGTCCTTTATGGTGGCCCTCACTAGCCATTTCCITTGACACAGTCGGTCTGGTCACT	710
LELYSTAD SEQ (13484-14089)	GTAATCCACTGCAAGATTGTTGGCGGGGGTAGGTACTCTGAGCGTCTACGGGCTTTGTGCTTTTCGCAAGCGTTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGTCTACCGCTGGGTTTGTTCACGGGGGTAATGTTCTGAGTAGCATGTACCGGCTCTGTGCCCTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GTAATGTTTGTGATCCGTGCTGCTGAAGAATTGCAATGCCCTGCGGTATGCCGTACCGGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGTGATATAGGCTTGGCAAGAATTGCAATGCTCTGGCTACTGATGTACCAAGATATACCAACTTTCCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATGGAAGTQTCGAATAGTTGGTAGAAAATTTGGGCAAAAGCCGAAATCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGCAGACTTCATCGTTGGCGTCCCTGCTGATCATATAGAAAAAGGGGCAAAAGTTGAGGTCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTTCGTACCAATCAAACATGTCTGCTCTGAAGGGGTTAAAGCTCAACCCCTTTACAGAGACTTCGGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCAACCTGATCGACCTCAAAGAGATTGTGCTTGATGGTTCGCGGGCT-AACCCCTGTTAACCAAGAGTTTCAGGGGA	1009
LELYSTAD SEQ (13484-14089)	GCAAATGGGAGCCCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTCGTCCTTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	AATCGAGTCG TCGTTAGATG ACTTGTGTCG TGATAGCAGG GGTCCACAAA AGTTCCTCTT -ATGG-SAGG --CGTAGAGG ATTITTTGCAA CGATCCTATC GCGGCACAAA AGCTCGTGGT	947 14132
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GGCGTTTCT ATTAACCTACA CCGCAGTTCAT GATATATGCC CTAAAGGTGA GTCCGGGGCG ACCGTTTACC ATCAGATACA CACCTATTAAT GATATAGCC CTAAAGGTGT CACCGGGCGG	1007 14192
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	ACTCTTAGGG CTCTCGCACC TTTTGGTCTT CTGAATTTGT GGTTTACCT TCGGTATCAT ACTCTCGGG CTGTTCGACA TCCCTAAATATT TCTGAACGT TCGTTTACAT TCGGATACAT	1067 14252
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GACATTCGTG CACTTTCAGA GTACAAATAA GTCCGGCTC ACTATGGGAG CAGTAGTTGC GACATATGTG CATTITCAAT CCACCAACCG TGTCCGACCTT ACCCTGGGGG CTGTTGTGCG-	1127 14311
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	ACTCTTTTGG GGGGTGTACT CAGG--CATTA GAACCTGGA AATTATATCAG CTCCAGATGC -CGCTTCTGT GGGGTGTCTTA CAGCTTCACA GAGTATGGA AGTTTATCAG TTCCAGATGC	1185 14370
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	CGTTTGTGCTT TGTAGGCG CAAGTACATT CIGGGCCCTG CCAACACAGT TCAAGTGGC AGATTGTCTT GCCTTGGCG CGGATACATT CIGGGCCCTG CCAATCAGT ACAAGTGGT	1245 14430
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	GCAGGCTTTTC ATCCGATTCG GGAAATGAT AACCAAGCAT TTTGTGTCG GCGTCCCGG GCAGGTCTCC ATTCAATCTC AGGTCTGCTT AACCAAGCAT ACGCTCTGAG AAAGCCCGGA	1305 14490
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	TCCACTACCG TCAACGGCAC ATTGGTCCC GGGTTAAAAA GCCTCGTGT TGGTGGCAGA CTACATACG TCAACGGCAC TCTAGTACCA GGAATTCGGA GCCTCGTGT TGGGCGCAAA	1365 14550
ISU 12/7a/3' terminal (888 - 1413) Lelystad seq (14077 - 14598)	AAAGCTGTTA AAAGGGAGT GGTAAACCTT GTTAAATATG CCAAAATAA CGAGCTGTTA AAGCAGGAGT GGTAAACCTT GTTAAATATG GCGGTAA	1413 14598

FIG.9

Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	ATGCCCGGTA AAAACCAGCA- -----AT	CCCACACAGAA GCCAAATTAAC	AAACAAAGT ACCGGAAGC	A-CAG-----C AGCAGAAGAG	14632 1434
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	TCCCATGGGG AAGCAAGGGG	AATGCCCAGC CAGTCAATCA GATGCCCAGC CAGTCAATCA	ACTGTCCCAG GCTGTGCCAG	TTCGTGGGTG ATGCTGGGT-	14681 1483
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	CAATCATATAA -AA-GATCAT	GTCACACCC CGGTCAACAA	CACCAACCTTA AACCACTCA	CGCG--A-CG GAGCAAGGG	14728 1528
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	AAGAAAAA-- AAGAAAAATA	----- AAGAAAAATA	CCATTTTC CCCGGAGAG	CCCTGGGTGG CCTATTTC	14766 1578
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	TGAAGATGAC TGAAGATGAT	ATCCCGCACC GTCAGACATC	ACCTACCCCA AGTTTACCCC	CACCTGACCC TAGTGAAGGT	14816 1628
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	TGCAATTCGAT TGTGCTCAAT	CCAGACGGGT CCAGACGGGC	TTCAATCAAG TTTAATCAAG	GGCGAGGAAG GGGTGGGAG	14865 1677
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	TTCATCCAGC GTCAGATTCA	GGCAAGGTCA GGGAGGATTA	GTTTTCAGGT GTTACACTGT	TCAGTTATG GGAGTTAGT	14915 1727
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	CTCATAACAGT ATCATACTGT	CGCCCTGATTT CGGCTGATC	CTACATCCGC CATCAACCG-T	CAGTCAGGGT CAG-CATIGA-	14965 1774
Lelystad seq (14588 - 14974) ISU 12/7a/3' terminal (1403 - 1774)	GCAAGTTAA				14974 1774

FIG.10

ISU 12/7a/3' terminal (1775 - 1938)	TCGGCTGGCA TTCTTGAGCC ATCCAGTGT TTGAATTGGA	1814
Lelystad seq (14975 - 15101)	14976
ISU 12/7a/3' terminal (1775 - 1938)	ACAAATGGTG GTGAATGGCA CTGATTGACA TTGTGCCCCTCT	1854
Lelystad seq (14975 - 15101)	TCACAGTCAG GTGAATGGCC GCGATTGGCG TGTGCCCCTCT	15016
ISU 12/7a/3' terminal (1775 - 1938)	AAGTCACCTA TTCAATTAGG GCGACCTGT GGGGCTAACA	1800
Lelystad seq (14975 - 15101)	GAGTCACCTA TTCAATTAGG GCGATCACAT GGGGCTCAATA	15056
ISU 12/7a/3' terminal (1775 - 1938)	TTTAATT-GG CGACAACCAC ACAGCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 - 15101)	CTTAATCAGG CAGCAACCAT GTACCGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 - 1938)	AAAAA	1938
Lelystad seq (14975 - 15101)	AAAAA	15101

FIG. 11

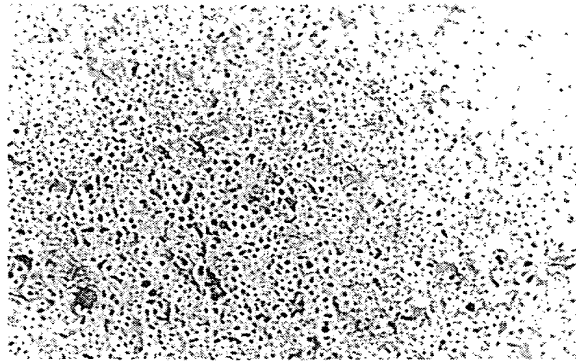


FIG. 12

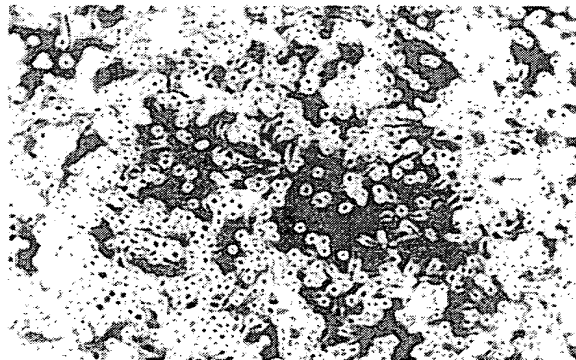


FIG. 13

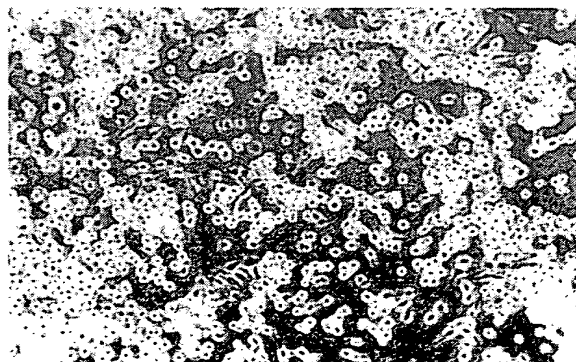


FIG. 14

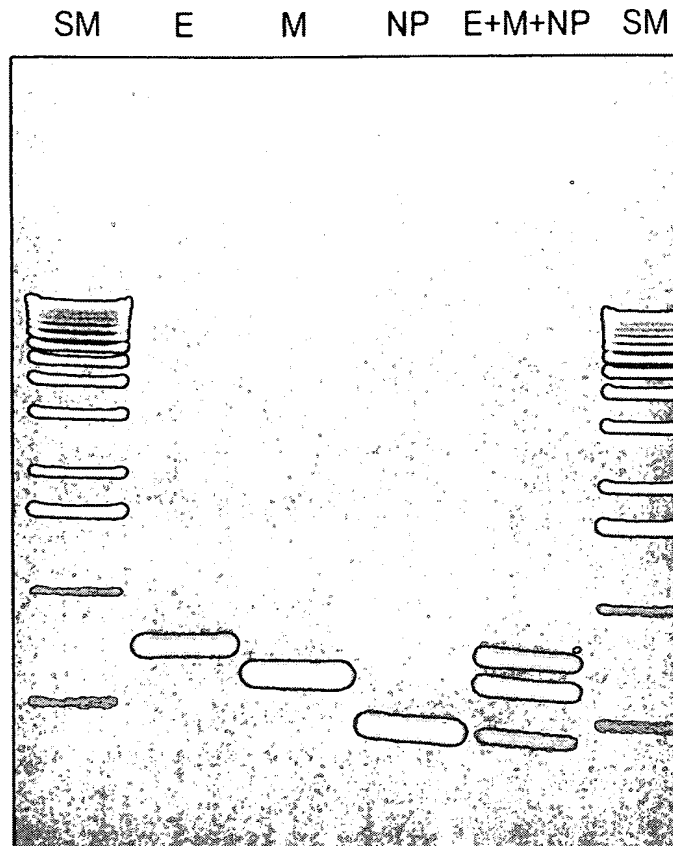


FIG. 15

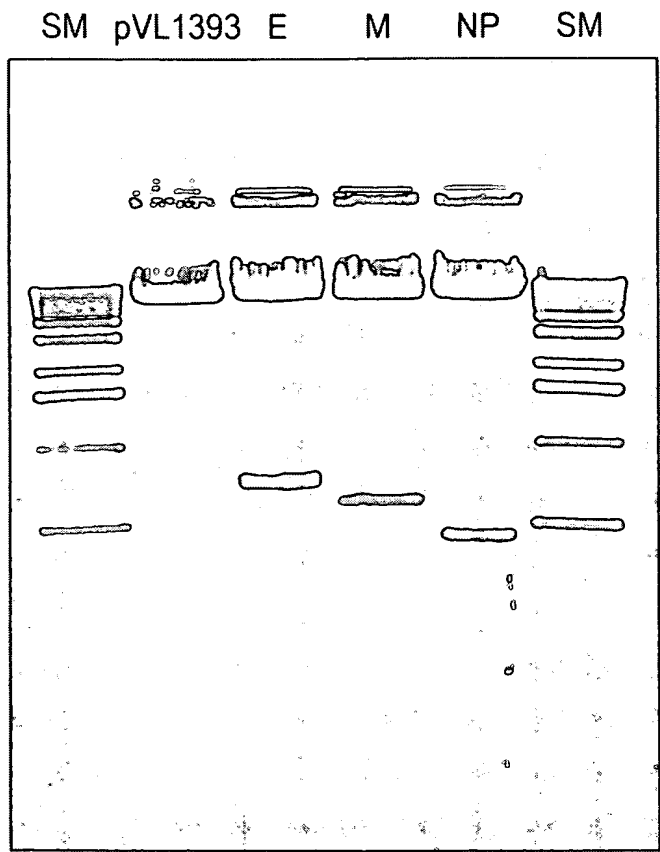


FIG. 16

DRF 6 start
+ 1>
VR 2385 AIGGAGTCGCTTAGATGACTTCCTGTCATGATAGCAGCGCTCCACAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGATGATATATGCC 100
ISU-1894C.....T..... 100
ISU-22C.....T..... 100
ISU-79T.....T.....A..... 100
ISU-55C.....T.....C..... 100
ISU-3927C.....T.....G.....T..... 100
LVG--A..-G..C.....C..T..TC..CG.....C..CG..GC..A..C..AGC..C..A.....A..TA..A.....C..... 97
VR 2385 TAAAGTGAGTCGGCGCGACTGCTAGGGCTTCGACCTTTTGGTCTTCCTGAATTGGCTTTCACCTTCGGGTACATGACATTCTGCGACTTTCAGAG 200
ISU-1894A..... 200
ISU-22A..... 200
ISU-79A..T.....C.....A..... 200
ISU-55A..A.....A.....A.....G..... 200
ISU-3927A.....A..T.....T.....T..... 200
LVTCA.....C..G.....GT.....A..CC..AA..A..T.....C..T..C..T..A.....A.....AT.....T.....ATC 197
VR 2385 TACAAATAAGTCGGCTCACTATGGGAGCAGTAGTTGCACTCCTTTGGGGGGGTGTACTCAGC--CATAGAAACCTGGAAATTCATCACCCTCCAGATGCC 298
ISU-1894 298
ISU-22A..... 298
ISU-79 298
ISU-55C..... 298
ISU-3927C.....C.....T.....C.....TTA.....TT..C..GT..A.....G..T.....T.....A 295
LVC..C..CCGT.....A..T..CC.....G..T..T..C..--..CCT..C..T.....TTA.....TT..C..GT..A.....G..T.....T.....A 295

FIG. 17A

FIG. 17B

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCACCAAAACCAGTCCAGAGGCAAGGGACCGGGAAAGAAAAAATAAGAGAAAAACCCGGGAGAGCCCCATTTC	679
ISU-1894--..-.....G.....C.....	679
ISU-22C--..-.....G.....T.....	679
ISU-79--..-.....C.,G.,.....T.,.....	679
ISU-55--..-.....G.,.....C.,.....	679
ISU-3927	...A.,.....--..-.....C.,G.,.....T.,.....	679
LVT.,.....GC.,T.,...A.AGT,C.,G.,---G.,...--,-,CCT,G.,...---,....C.,---GCC,A.,.....G.,T.,.....A.,...T	679

FIG. 17C

VR 2385	CTTGACC-CTGTCAGATTTCAGGAGGATAAGTTACAC	CTGGAGTTAGTTGCCTACGCATCATACTGTGGCCCTGATCCGGGTCACAGCATCACCC-	877
ISU-1894T.....	877
ISU-22A.....	877
ISU-79T.....	877
ISU-55T.....G.....G.....	877
ISU-3927C..T..T..A.....G.....T.....G..C.....	877
LVGT..G..T...TCCAGC...A..G..C...TTCAG..T.....TGC...GGTTGC.....A.....T.....G..TT..TA..T..G		878

VR 23 85	TCAG-CA-----TGA	*** DRF 7 stop	886
ISU-1894		886
ISU-22		886
ISU-79		886
ISU-55		886
ISU-3927		886
LV	C...T...GGGTGCAAGT..A. AAAAAAAAAAAA		898

FIG. 17D

VR 2385 DRF6	MESSLDDFCHDSTAPQKVLLAFSITYTPVMIYALKVSRGRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWGVYSAIETWKFITSR	100
ISU-1894 DRF6	.G.....I.....	100
ISU-22 DRF6	.G.....I.....	100
SIU-55 DRF6	.G.....I.....	100
ISU-79 DRF6	.G.....Y.....M.....	100
ISU-3927 DRF6	.G.....N.....E..R.....	100
LV DRF6	.G-G.....N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S.....	99
PRRSV-10 DRF6	.G-G.....N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S.....	99
LDV-C DRF2	.G-G.-E..DQTSWY.-IFI...L...IA.S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLVKIVDWLVI...	96
LDV-P DRF2	.G-G.-E..DQTSWY.-I.I...L...IA.S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..T...SL...I..V..I.TLVKIVNWMVL...	96
VR 2385 DRF6	LCLLGRKYILAPAHHVESAGGFHP1AANDNH-----AFVRRRPGSTTVNGTLVPLKSLVLGGRKAVKQGVVNLVKY-AK	183
ISU-1894 DRF6-----	174
ISU-22 DRF6-----	174
SIU-55 DRF6-----	174
ISU-79 DRF6-----	174
ISU-3927 DRF6-----R.....K.....	174
LV DRF6	..C...R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR...R.....-GR	173
PRRSV-10 DRF6	..C...R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR...R.....-GR	173
LDV-C DRF2	..F...S.....PS.,D-----TSDGRQSLTTSLT..K...L...Q...DFQR.....K...SK.A...L..VS.	171
LDV-P DRF2	..F...S.....PS.,D-----TSDGRQSLTTSSTT.....K...L...Q...DFQR.....K...SK.A...L..VS.	171

FIG. 18A

VR 2385 DRF7 MPNNTGKQQRKK-----GDGQPVNQLCQMLGKIIAHQNSRGKGPCKKKNKKNPEKPHFPLATEDDDVRHHFTPSEKQLCLSSIQTA FNQAGTCTLS 100
ISU-1894 DRF7N.....Q..... 93
ISU-22 DRF7N.....Q..... 93
ISU-79 DRF7N.....Q..... 93
ISU-3927 DRF7N..K.....Q.....I.. 93
ISU-55 DRF7N..K.....Q.....SG..... 93
VR2332 DRF7N..TEE.....Q..... 93
LV DRF7--A..N..SQ..KKSTAPM..N.....L..AM..KS..R..---QPR..GQA.....K.....A.....I.....L..QT.....S.....Q.....AS.. 94
PRRSV-10 DRF7--A..N..SQ..KKSTAPM..N.....L..AM..KS..R..---QPR..GQA.....K.....A.....I.....L..QT.....S.....Q.....PS.. 94
LDV-C DRF1SQ..KK..GGQN.....AN.....N..LISALLRNAG.....--N..K..Q..K.....-Q..-L.....M..GPS..L.....VM.....N..V..M..R.....LV..L.....G..Q.....V 85
LDV-P DRF1SQ..KK..SGQN.....AN.....N..LINALLRNAG.....--N..K..Q..K.....-Q..-L.....M..GPS..L.....VM.....N..V..M..R.....LV..L.....G..Q.....V 85
EAV DRF7ASRRSRP..AASF-----RN..R--RRQPTSVDLLRMFG.....-----MRVR..PPAQPTQAI..EPG..L.....DLNQQ.....ATLS..NV..RF..MI..H..SL..-A 83
^^^^^^

VR 2385 DRF7 DSGRISYTFESLPHTHTVRLIRVTASP-----SA 134
ISU-1894 DRF7123 123
ISU-22 DRF7123 123
ISU-79 DRF7123 123
ISU-3927 DRF7P.....123 123
ISU-55 DRF7123 123
VR2332 DRF7123 123
LV DRF7 S..KV..FQ...M..VA.....STSASQAS 128
PRRSV-10 DRF7 S..KV..FQ...M..VA.....STSASQAS 128
LDV-C DRF1G..NF...S..M.....A.....NAS..NS----- 115
LDV-P DRF1G..NF...S..M.....A.....NAS..NS----- 115
EAV DRF7A..GLT....SW-V..KQIQ..KVAPP..G.....- 110
^^^^

FIG. 18B

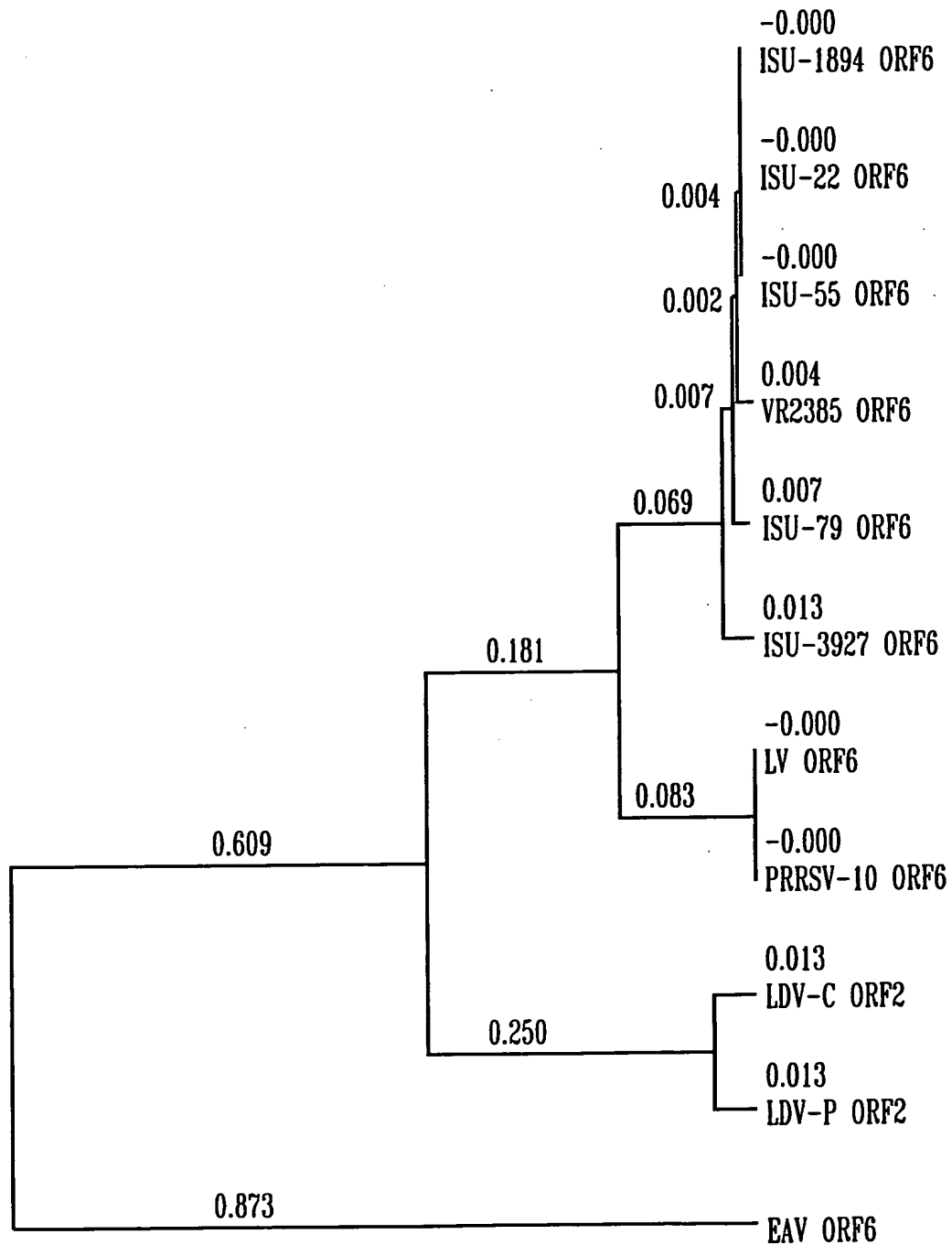


FIG. 19A

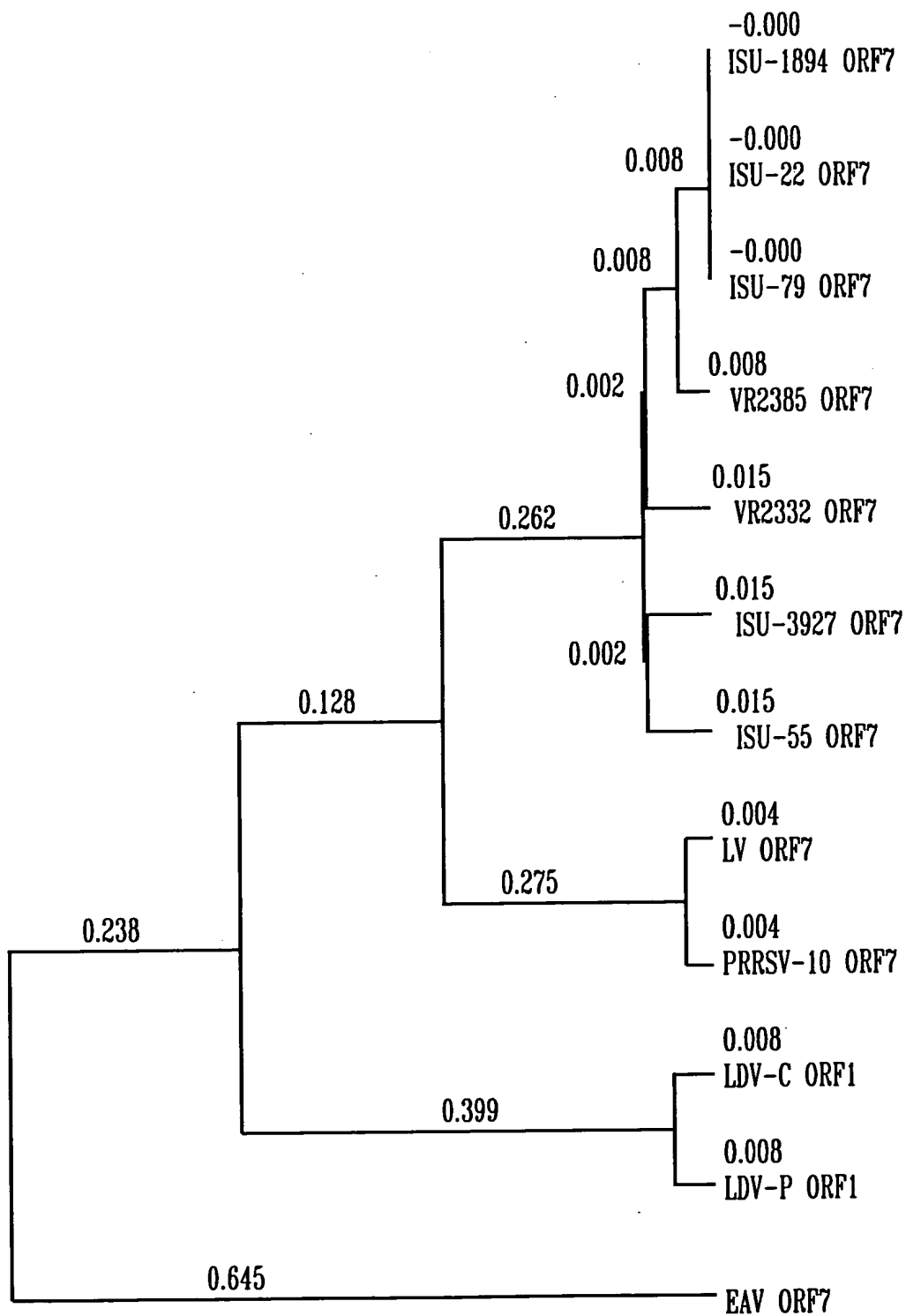


FIG. 19B

+ Start DRF2
100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGACAAATTGGCCAACCTTTTGTGGATGCTTTCACGGAGTCTTGGTGCCATTGTTGAT
200 ATCATTATATTTTGGCCATTTTGTGGCTTACCATTGCAGGTTGGCTGGTCTTTTGCATCAGATTGGTTTGTCTCCGGGATACICCGTGGCGGCC
300 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCCTTCTCTCAGTGCCAGGTGGACATTCCCACCTGGGGAACTAAACATCCTTTTGGGGA
400 TGCCTTGGCACCATAAGGTGTCAACCCTGATTGATGAAAATGGTGTGGCTCGAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCTGGAAACAGGT
500 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTCAGCATCTTGCCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC
600 TCTCGGCTGCCCATGCTACACCACCTGGCGATGACAGGGTCAAAATGAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTGTCTTTTCCCAACCC
+ Start DRF3
700 CTGTTCCCGGCAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTATATTTTCCCTGTTCAGCTTCTTGTACTCTTTTGTGTGT
*** Stop DRF2
800 GCTGTGGTTGCGGGTCCAAATGCTACGTACTGTTTGGTTTCCGCTGGTAGGGCAATTTTCTTCGAACCTCAGGTGGAATTACACGGTGTGCCGC
900 CTTGCCCTACCCGGCAAGCAGCCGAGAGGCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGCGATGATCGATGTGGGAGGACGATCATGATGA
1000 ACTAGGGTTGTGGTGGCGTCTGGCCCTCTCCAGCGAAGGCCACTTGACCAGTGCTTACGGCTGGTTGGCGTCCCTGTCTTCAGCTATAGGCCAGTTC
1100 CATCCCGAGATATTCGGGATAGGGAAATGTGAGTCGAGTCTATGTTGACATCAAGCACCATTCAATTTGGCTGTTTCATGATGGGAGAACACCACCTTGC

FIG. 20A

+ Start DRF4
CCCACCATGACAACATTTCAGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTTCACCTAGATGGGTGGTCCCTTCCTTTTC 1200
CTCTTGGTTGGTTTTAAATGTCCTCTTGGTTTCTCAGGCGTTCGCCTGCAAGCCATGTTTCAGTTCGAGTCTTTTCAGACATCAAGACCAACACCACCGCAG 1300
*** Stop DRF3
CGGCAGGCTTTGCTGCTCCTCCAAGACATCAGTTGGCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGCCGCGACGGGATAGG 1400
GACACCGGTGTATCACTGTCACAGCCAATGTTACCGATGAGAAATTATTGCAATCCCTCTGATCTTCATGCTTTCTTCCTTTCTATGCTTCT 1500
GAGATGAGTGAAAGGGATTTAAGGTGGTATTGGCAATGTCAGGCATCGTGGCAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTCAGGAAT 1600
TTACCCACGTTCCCTGGTAGTTGACCATGTGCGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCACTGTTTAGCCTGCTCTTTTACCAT 1700
*** Stop DRF4 + Start DRF5
TCTGTTGGCAATTGAAATGTTAAGTATGTTGGGGAAATGCTTGACCGGGGCTGTGCTCGCAATTGCTTTTTTAAGGTGATCGTGCCGCTTGT 1799

FIG. 20B

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTGTGAYAAAATYRGCCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...T...G...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...G...C...C...T...T...TAGTG...G...TGGC...T...	91
Consensus	YYTKGCCATWYGTGGSTTACCRTCCGAGGWTGGYTRSTGGTCTTTYKMYTCAGAKTGGTTTGCTCCGGMTWCTCCGTKGGCGCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...A...T...C...GG...TGCA...T...T...A...A...G...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...T...	191
Consensus	TCTSMSSAAYTAYMGAGRTCTATGARGSCCTTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKGSARYAARCAAYCCWTTGGGKATGYTTGGCA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...TC...G...CAGGT...C...T...-C...GG...G...ACT...A...T...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMCYTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAAMWKCAGGWARGCKGCCCTGGAARCAGGTRGTRGYGA	400
VR2385 DRF2	...AA...-...G...AAC...C...A...G...G...A...G...A...G...GC...T...A...G...T...A...A...A...GA...C...	398
LV DRF2	...-...GC...T...CCA...T...G...C...C...T...A...G...C...TT...T...A...G...G...G...G...TG...T...	389
Consensus	GGCYACGCTSTCWGMAKYWGTCAAGKYTSGATRTGTRGTRKTRCTCATTTTCARCAYCTKCCGCMRTKGARGCSGAKWCTGYMRMTWTCTSRSCTCWGR	500
VR2385 DRF2	...T...G...T...C...TTA...-...TT...G...G...G...G...T...T...T...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...A...C...G...AG...G...G...TT...T...CCGC...T...CAG...A...A...	487

FIG. 21A

Consensus	TSSYSATGCTAMAMMAYCTGYGCAYGWAAGGTCAAATGTRASCMTASWGTAYAAAYACKTTGRAYCRSGTGTKWGTCTRTYTTCCCMACSCCWGGTW	600
VR2385 DRF2	.GCCC.....C.CC.C...C...T.AC.....A.C.A..GT...T..T.GT...T...A.T.AG...TT...-G.T.....A..C..T...T	595
LV DRF2	.CGTG.....A.AA.T...-T...-C.TT--..-.....G.G.C..CA...C..C.CC..G...G.C.GC..-GA.....A.C.....C..G..A...A	580
Consensus	CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMATMRSTGTRCAYKCYTCYATWTTTCCCTCTGKGCWKCTCKKTACYYTKTTYRTWGTGCTKIG	700
VR2385 DRF2	.CC...A...C.TCAT.....CAG.....A..AGC...A..TT.C..T..A.....T...AG.T...TG...TC.T..TG.T.....G..	695
LV DRF2	.GA...C...T.GACC.....AGA.....C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTTCCARYKCTACGYWMTGTTTTTGGTTCCRYTGGYMRSGGCAAYWYWTGTTTGGARCTACGGTGA	776
VR2385 DRF2	.T.G..GG.....ATG.....TAC.....GC...TAGG.....TTTT..T.....A..C.....	771
LV DRF2	.C.T..AA.....GCT.....CTA.....AT...CCCAC.....CACA..A.....G..G..-----	750

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGRCAYKCYTCYATWTTTCCCTCTGKGGKWCWCTCKKTACYYTKTYRTWGTGCTKGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3C..CAG...G..CG..T..C..T.....G..TT..A...GT...CT..G..CA..A...T...C..T..AA.....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT..C..T..A.....T..AG..T...TG...TC..T...TG...T...G...T..G...GG.....ATG.....TAC....	100
Consensus	TTTGGTTCCRYTGGYMRSGGCAAYWYWCWTTTCGARCTSACTSAAYTACACSRTRTGCMYGCCYTGYYACCMGKCAAGCGCTCGCMRARGSCT	200
LV DRF3AT...CCCAC.....CACA..A.....G...G..CA..C...C.....CA..A...AT...C..TTCT...A..T.....G.....CA..A..G..	200
VR2385 DRF3GC...TTAGG.....TTTT..T.....A..C...GG..G..T.....GG..G...CC...T...CCTC...C..G.....A...-...AG..G..C..	199
Consensus	ACGARCCCGGMYGKWMCMTKTGGTGCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCRSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	...G....TC..TAA..A..G.....AA.....CA..G....A...CGT..C.....GT..-TTAA...CA..C.....C..GTA..GA..	298
VR2385 DRF3A....CA..GTC..C..T.....GG.....TC..A....G....GAC..T.....AC...GGTT...-GG..G.....T...CCT..TC..	298
Consensus	SRCGAMKSMMACTTGACSRGTMATTAYGCTGGYTGCKTYYYTGCTTYWVSCATYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGTGWS	400
LV DRF3	A..--CTCAA.....-GG..TA...T..T...C...T..TTT.....TTC...CG.....A.....G...T..G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T....G..CCC.....CAG...TA.....G.....C...A..A.....AG	398
Consensus	KCGMGTCTWGTGACAWSMRRCACCARTTCATTGTGCGYGWKCATGATGGRCASAAVWCMACCKTRYCYMMCSRWSACACATYTCMGCMKTRYWTSMG	500
LV DRF3	G..C....TC..G...AGCGA.....G.....T..C..AG.....T..C..AG.....A..C..TT..A...G..AT..TAC..GGAC.....C..C..AT..ATA..GC..	495
VR2385 DRF3	T..A....AT..T....TCAAG.....A.....C..T..TT.....G...G..CA..C...T..GC..CCA..CATG.....T..A...CG..GCT..CA..	498

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTYCAYYTRGAATGGSTGGCKCCMYTCTTTTCYTCYTGGTGTYMAAYRTMTCTGTTTC	600
LV DRF3	G. A. C. C. AA. A. C. TT. G. C. G. AC. T. C. C. GC. C. . CA. A. . A.	595
VR2385 DRF3	A. C. G. T. GG. C. T. CC. A. G. T. CT. C. T. TT. A. . TG. C. . T.	598
Consensus	TSAGGGCTTGGCTGYAAGCCMTGTTTCWSKWCGMRCTCTWTGAGATYRAGACCAACACACCGCGCGCMGGYTTYRYKGTCTTCYARGACATCART	700
LV DRF3	. G. T. C. TCGA. CA. . A. T. TG. G. G. T. C. T. . CATG. T. G. A.	695
VR2385 DRF3	. C. C. A. AGTT. . AG. . T. C. CA. C. A. G. A. C. . TGCT. C. A. G.	698
Consensus	TGYTYMGRMTCACGGSRWCTCRGACGCKCANGAGRMRAATTCCTTCGSAAGTCGYCYCARTGCGYGAMGCGWYRGTACTCCCCAGTACATCAGCA	800
LV DRF3	. . TT. CC. A. C. GGT. . A. G. A. . AAA. G. T. C. A. . T. . A. C. . TCG.	795
VR2385 DRF3	. . CC. TA. G. A. . ---. CAA. . G. . --. T. -T. . GCG. ----. C. -C. T. G. C. . C- C. G. . ATA. -----	765
Consensus	TAA	803
LV DRF3	...	798
VR2385 DRF3	---	765

FIG. 21B.1

Consensus
VR2385 DRF4
LV DRF4
ATGGSTGGCKCCMYCTCTTTTCYTCYTGGTGGTKYTMAYRTMTCWTGGTTCTSAGGCGTTCGCCCTGYAAGCCMTGTTTCWSKWCGRMRTCTWTCAGAYA
....G....T..CT.....C..T..T...TT.A.,TG.C.,T.....C.....C.....A.....AGTT..AG...T.....C.,
....C....G..AC.....T..C...C....GC.C.,CA.A.,A.....G.....T.....C.....TCGA..CA...A....T.,
100

Consensus
VR2385 DRF4
LV DRF4
TYRAGACCAACACACCGCRGCKGCMGGYTYRYKGTCTCYCARGACATCARTTGYTYMGRMTCACGSRWCTCRGCAGCKCAWGAGMRATTTCCCTT
..CA.....C.....A.,G.,A.,C.,TGCT.....C.,A.....G.,CC.TA.G.A.,---,CAA...G.,-T.,-T...GCG,-----,
189
..TG.....G.....G.,T..C.,T.,CATG.....T..G.....A...TT.CC.A.C.....GGT...A.....G.,A....AAA.....
200

Consensus
VR2385 DRF4
LV DRF4
CGSAAAGTCGYCARTGYCGYMRGCSRTMGGKACWCCSWGATAYATCACKRTMACRCGYAAYGTACCGAYGARWMTAYTTGYAYWCKCKGAYCTK
..C.....-C.T.,G.,C.,CAGG.,GA.A.,G.,A.,GT...T.....TG.C.,A.,C.,T.,T.....T...GAAT...T...C.TTC.T.,T.,T...T
288
..G.....T.C.,A.,T.,TGAA.,CG.C.,T.,T...CA...C.....GA.A.,G.,T.,C.,G.....C...ATCA..C...T.CAA.G.G.,C...G
300

Consensus
VR2385 DRF4
LV DRF4
CTSATGCTTCTCKCTGCCTTTCTAYGCYTCWGATAGYGAARGGMTTYAARGTSRTMTTGGSAATGTSTCWGGCRTYGTKKCWGKTGYGTCA
..C.....T.,T.....T.,T.,T.,G....T.,A.,G.,A.,T.,G.,GG.A.....C.....G.,A...A.C.,GG.A.TG.,C....
388
..G.....G.G.....C.,C.,A.,A.....C.,G.,A.,C.,C.,A.,CA.C.....G.....C.,T...G.T.,TT.T.CT.,T....
400

Consensus
VR2385 DRF4
LV DRF4
AYTTCAMRRTTAYGTSSMMCATGTCAAGGAATTTACCCAACATACCCAGCAGYATCAYYTGGTARTTGAYCAYRTKGGYTGCTSCATTTCMTGACRCC
..C.....CAG...C.,CCAA.....-----,T-,-CT.....G....C.,TG.G...C....C.....A...G..
500
..T.....AGA...T.,GGCC.....-----,C....TC.....A.....T.,CA.T...T....G.....C....A..
476
491

Consensus
VR2385 DRF4
LV DRF4
MKMKRCMATGAGGTGGGCWACRYWYTWGCTGTGTYKTYRCCATTCTCTTGGCAATWTGA
CGAGA.C.....A.,TGTTT.A.,C...C.T.,TA.....G.....T...
561
537
552
ATCTG.A.....T.,AACCA.T.,T...T.G.,CG.....C.....A...
561
537
552

FIG. 21C

Consensus	M, WG, C, . K, L, W, L, SL, P, CL, SPSQ, G, WSF, S, WFAPR, SVRALPFTL, NYRRSYE, L, C, D, P, KH	100
LV DRF2,	. Q, . H, GV, SASCSWTPS, SSSLV, LI-----, PF, Y, G, D, Y, F, E, P, GL, PN, RP, V, QFAV, . .	90
VR2385 DRF2,	. K, . L, --, ----AFLTK, AN-FL, MLSSSWCP, LI, YFW, F, A, D, Y, S, AF, SQ, QV, I, TWGT, . .	93
Consensus	PLGM, WH, . VS, LIDEMVSRR, Y, . ME, . . GQAANKQVV, EATL, S, LD, V, HFQHLAA, EA, C, L, SRL, ML, NV, YN, TL, V,	200
LV DRF2, F, MR, . H, I, QT, . HS, G, TKL, G, . I, T, V, DS, RF, S, V, KN, AV--G, . SLQ, . T, . . DR, ELI	188
VR2385 DRF2, L, . HK, . T, M, RI, . KA, S, SRI, S, . V, A, I, . ET, KY, A, P, HH, RMTGS, . TIV, . S, . . NQ, FAV	193
Consensus	FPTPG, RPKL, DF, QWLI, VH, SIFSSVA, S, TLF, VLWLR, P, LR, VFGF, W, A,	264
LV DRF2, T, T, R, S, A, S, V, I, I, A, Y, H, PT, ---THSS	249
VR2385 DRF2, S, H, Q, A, S, A, C, V, V, M, T, R, LG, IFLNSNR-	257

FIG. 22A

Consensus MA, C, ..., FLC, ..., Y, ..., A, ..., S, T, CFWFPL, GN, SFELT, NYT, C, PC, T, QAA, ..., EPGR, WC, IGHDR, E, DHDEL, ..., PSG, ..., 100
 LV DRF3, ..., HQ, ARFHF, ..., GFIC, LVHS, LASN, SS, L, ..., AH, T, ..., I, M, S, S, RQRL, ..., NM, K, ..., E, R, ..., LMSI, ..., YDN 100
 VR2385 DRF3, ..., NS, TFLYI, ..., CSFL, SFCC, WVAG, NA, Y, ..., VR, F, ..., V, V, P, L, R, AEAY, ..., SL, R, ..., G, D, ..., GFVV, ..., LSS 100

Consensus ..., L, ..., YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD, HQFICA, HDG, N, T, ..., NISA, ..., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL 200
 LV DRF3, L-K, EGY, ..., F, ..., A, ..., L, ..., F, KR, ..., E, H, S, VSTGH, ..., LYAA, H, I, ..., L, ..., I, ..., 199
 VR2385 DRF3, EGH, TSA, ..., S, ..., T, ..., I, ..., Y, IK, ..., V, Q, T, LPHHD, ..., VLQT, Q, V, ..., V, F, ..., V, ..., 200

Consensus RRSP, S, VS, R, Q, RPT, P, ..., S, TS, ..., L, ..., R, F, ..., K, S, ..., 266
 LV DRF3, ..., V, P, R, IY, IL, ..., R, RLPVSW, FR, IVSD, TGSQQRK, K, PSESPPNVW, P, VLPSTSR 265
 VR2385 DRF3, ..., A, H, V, VF, TS, ..., P, QRQALL, SK, V--A, GIATRPL, R, A-----, -, LSAARR- 255

FIG. 22B

Consensus M, A, L, F, L, G, ..., VS, AFACKPCFS, LSDI, TINTAAGF, VLQDI, C, R, ..., A, E, I, K, QCR, A, GTP, YIT, TANVTDE, YL, ..., DL 100
 LV DRF4, A, AT, F, A, AQHIM, E, ..., TH, E, ..., M, N, F, PHGVA, Q, K, SFG, SS, E, V, Q, I, ..., S, YNA, ... 100
 VR2385 DRF4, G, SL, L, V, FKCLL, Q, ..., SS, K, ..., A, S, L, HR--NS, S, A, R--, VP, T, I, V, V, ..., N, HSS, ... 96

Consensus LMLS, CLFYASEMSEKGFV, FGNVSG, V, CVNFT, YV, HV, ..., TQ, V, ..., RLLHF, TP, MRWAT, ACLF, ILLAI, 184
 LV DRF4, A, A, ..., I, V, SA, D, A, TQH, QHHL, IDHI, L, SA, TI, A, ... 183
 VR2385 DRF4, S, V, ..., I, AV, S, Q, KEF, RSLV, DH-V, M, ET, VL, T, ... 179

FIG. 22C

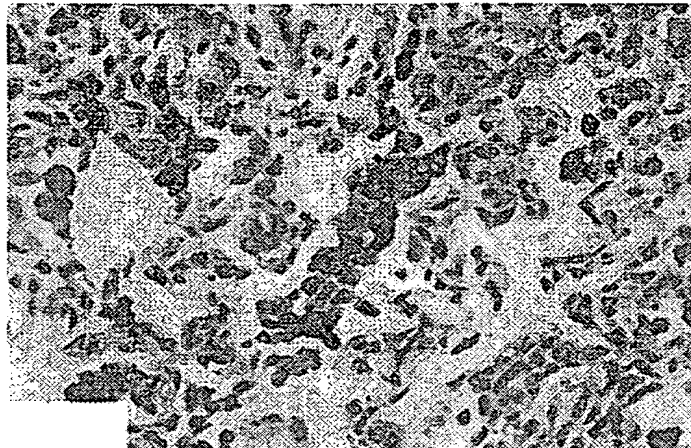


FIG. 23

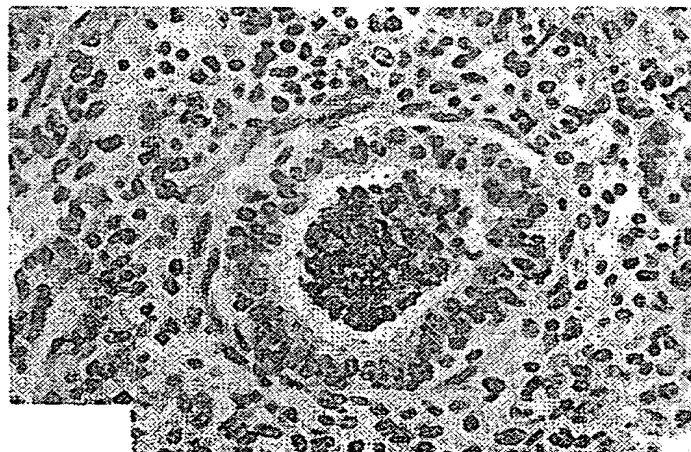


FIG. 24

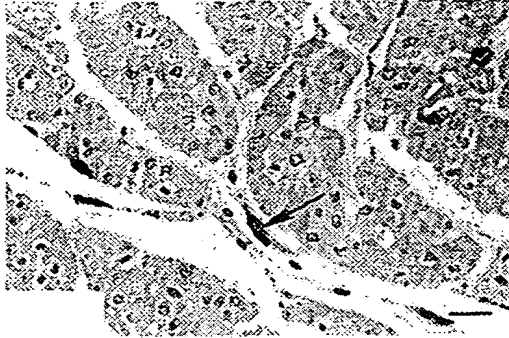


FIG. 25

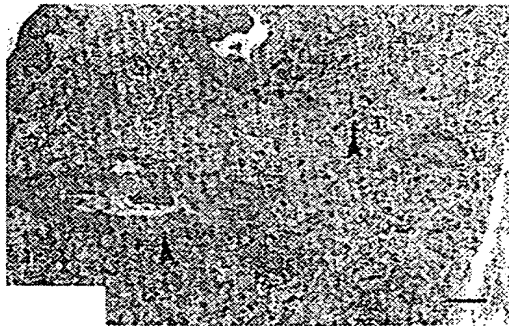


FIG. 26

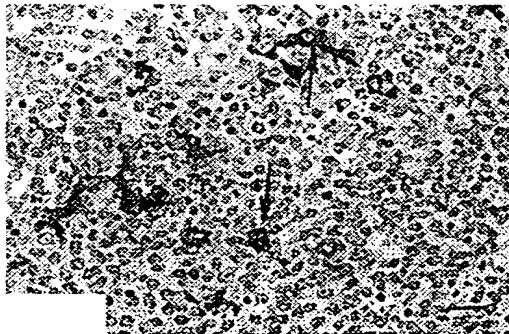


FIG. 27



FIG. 28A

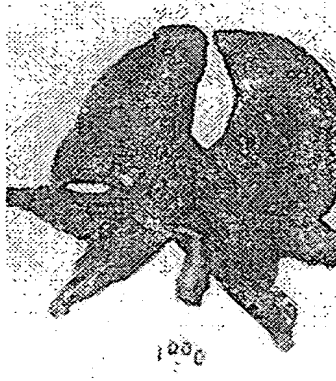


FIG. 28B

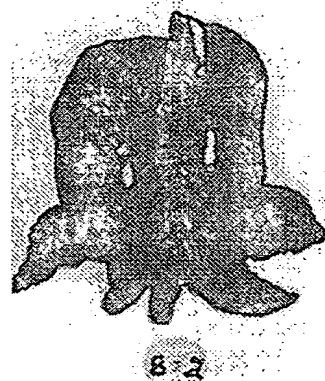


FIG. 28C

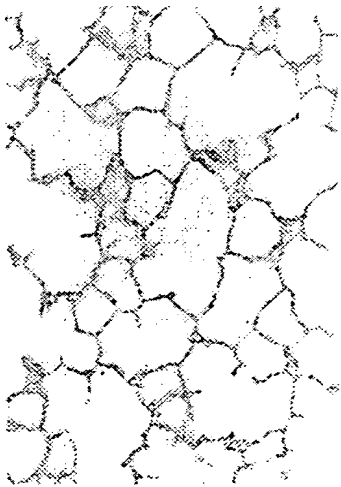


FIG. 29A

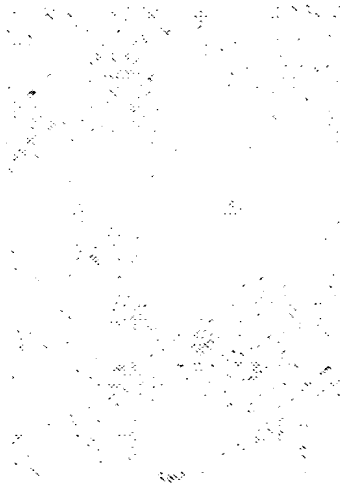


FIG. 29B

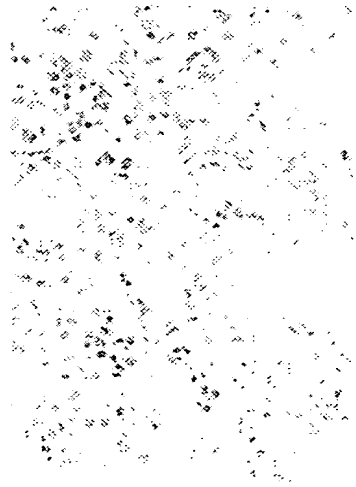


FIG. 29C

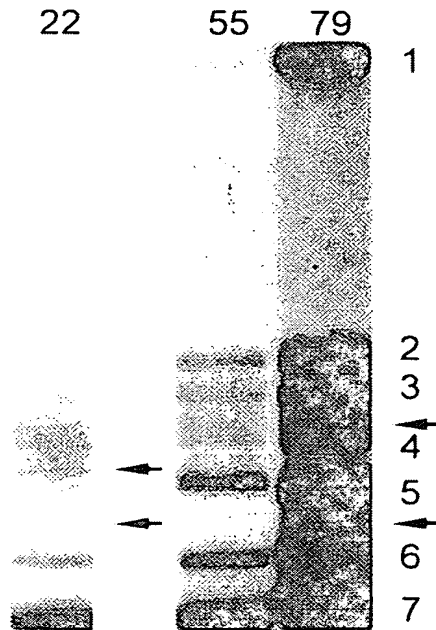


FIG. 30A

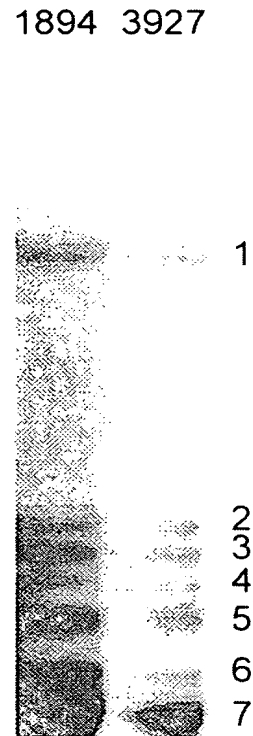


FIG. 30B